

SEQUENCE LISTING

<110> ROSENBLUM, MICHAEL G.
CHEUNG, LAWRENCE

<120> MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
MAKING THEEOF

<130> CLFR:007US

<140> UNKNOWN

<141> 2002-02-12

<150> 60/268,402

<151> 2001-02-12

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 316

<212> PRT

<213> Gelonium multiflorum

<400> 1

```
Met Lys Gly Asn Met Lys Val Tyr Trp Ile Lys Ile Ala Val Ala Thr
  1              5              10              15

Trp Phe Cys Cys Thr Thr Ile Val Leu Gly Ser Thr Ala Arg Ile Phe
              20              25              30

Ser Leu Pro Thr Asn Asp Glu Glu Glu Thr Ser Lys Thr Leu Gly Leu
              35              40              45

Asp Thr Val Ser Phe Ser Thr Lys Gly Ala Thr Tyr Ile Thr Tyr Val
              50              55              60

Asn Phe Leu Asn Glu Leu Arg Val Lys Leu Lys Pro Glu Gly Asn Ser
              65              70              75              80

His Gly Ile Pro Leu Leu Arg Lys Lys Cys Asp Asp Pro Gly Lys Cys
              85              90              95

Phe Val Leu Val Ala Leu Ser Asn Asp Asn Gly Gln Leu Ala Glu Ile
              100              105              110

Ala Ile Asp Val Thr Ser Val Tyr Val Val Gly Tyr Gln Val Arg Asn
              115              120              125

Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu Gly Leu
              130              135              140

Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser Tyr Pro
              145              150              155              160

Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu Gly Ile
```

	165		170		175
Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala Ile Asp	180	185	190		
Asn Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val Ile Gln	195	200	205		
Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln Ile Arg	210	215	220		
Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile Ser Leu	225	230	235	240	
Glu Asn Lys Trp Gly Lys Leu Ser Phe Gln Ile Arg Thr Ser Gly Ala	245	250	255		
Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn Gly Lys	260	265	270		
Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile Ala Leu	275	280	285		
Leu Lys Phe Val Asp Lys Asp Pro Lys Thr Ser Leu Ala Ala Glu Leu	290	295	300		
Ile Ile Gln Asn Tyr Glu Ser Leu Val Gly Phe Asp	305	310	315		

<210> 2
 <211> 1176
 <212> DNA
 <213> Gelonium multiflorum

<400> 2

cagcttctca	cttgtttggg	ataatgaaag	ggaacatgaa	ggtgtactgg	attaagattg	60
ctgtggcgac	atggttttgc	tgcactacta	ttgtacttgg	atcaacggcg	aggattttct	120
ctcttcccac	aaatgatgaa	gaagaaacca	gtaagacgct	tggcctggac	accgtgagct	180
ttagcactaa	aggtgccact	tatattacct	acgtgaattt	cttgaatgag	ctacgagtta	240
aattgaaacc	cgaaggtaac	agccatggaa	tcccattgct	gcgcaaaaaa	tgtgatgatc	300
ctggaaagtg	tttcgttttg	gtagcgcttt	caaatagaca	tggacagttg	gcggaaatag	360
ctatagatgt	tacaagtgtt	tatgtggtgg	gctatcaagt	aagaaacaga	tcttacttct	420
ttaaagatgc	tccagatgct	gcttacgaag	gcctcttcaa	aaacacaatt	aaaacaagac	480
ttcatttttg	cggcagctat	ccctcgctgg	aaggtgagaa	ggcatataga	gagacaacag	540
acttgggcat	tgaaccatta	aggattggca	tcaagaaact	tgatgaaaat	gcgatagaca	600
attataaacc	aacggagata	gctagttctc	tattggttgt	tattcaaagt	gtgtctgaag	660
cagctcgatt	cacctttatt	gagaaccaa	ttagaaataa	ctttcaacag	agaattcgcc	720
cggcgaataa	tacaatcagc	cttgagaata	aatggggtaa	actctcgctc	cagatccgga	780
catcaggtgc	aaatggaatg	ttttcgaggg	cagttgaatt	ggaacgtgca	aatggcaaaa	840
aatactatgt	caccgcagtt	gatcaagtaa	aacccaaaat	agcactcttg	aagttcgctc	900
ataaagatcc	taaaacgagc	cttgctgctg	aattgataat	ccagaactat	gagtcattag	960
tgggctttga	ttagtacaac	ttattgtgct	ttttatatat	tatagatatg	atgccggggc	1020
atgtattggc	cttcgtagct	taaataaagg	catcgaatat	tagcctcggt	ggtgtatcta	1080
tcatgctgtg	ttgtaaaact	gccaatgttt	atgttatcaa	acagaaattg	gcatgaagtt	1140
tctgtacaag	tgttcaataa	actgggctat	acatgc			1176

<210> 3
<211> 33
<212> DNA
<213> Homo sapiens

<400> 3
gctgcccaac cagccatggc ggacattgtg atg 33

<210> 4
<211> 50
<212> DNA
<213> Homo sapiens

<400> 4
gccggagcct ggcttgcacg ctgccgctgg tggagccttt gatcatccag 50

<210> 5
<211> 45
<212> DNA
<213> Homo sapiens

<400> 5
aagccaggct ccggcgaagg cagcaccaaa ggcgaagtga aggtt 45

<210> 6
<211> 30
<212> DNA
<213> Homo sapiens

<400> 6
gccaccgcca ccactagttg aggagactgt 30

<210> 7
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 7
ggcgggtggct ccgtcatgac ggacattgtg atgacccagt ctcaaaaatt c 51

<210> 8
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

Primer

<400> 8

ggtaggcggtg gctccggtct agacaccgtg acg

33

<210> 9

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 9

aaggctcgtg tcgacctcga gtcattaagc tttaggatct ttatc

45

<210> 10

<211> 1527

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<220>

<221> CDS

<222> (1)..(1521)

<400> 10

atg	acg	gac	att	gtg	atg	acc	cag	tct	caa	aaa	ttc	atg	tcc	aca	tca	48
Met	Thr	Asp	Ile	Val	Met	Thr	Gln	Ser	Gln	Lys	Phe	Met	Ser	Thr	Ser	
1				5					10					15		

gta	gga	gac	agg	gtc	agc	gtc	acc	tgc	aag	gcc	agt	cag	aat	gtg	gat	96
Val	Gly	Asp	Arg	Val	Ser	Val	Thr	Cys	Lys	Ala	Ser	Gln	Asn	Val	Asp	
			20					25					30			

act	aat	gta	gcc	tgg	tat	caa	caa	aaa	cca	ggg	caa	tct	cct	gaa	cca	144
Thr	Asn	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Glu	Pro	
		35				40						45				

ctg	ctt	ttc	tcg	gca	tcc	tac	cgt	tac	act	gga	gtc	cct	gat	cgc	ttc	192
Leu	Leu	Phe	Ser	Ala	Ser	Tyr	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	
	50					55				60						

aca	ggc	agt	gga	tct	ggg	aca	gat	ttc	act	ctc	acc	atc	agc	aat	gtg	240
Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Asn	Val	
	65				70				75					80		

cag	tct	gaa	gac	ttg	gca	gag	tat	ttc	tgt	cag	caa	tat	aac	agc	tat	288
Gln	Ser	Glu	Asp	Leu	Ala	Glu	Tyr	Phe	Cys	Gln	Gln	Tyr	Asn	Ser	Tyr	
				85				90						95		

cct	ctg	acg	ttc	ggg	gga	ggc	acc	aag	ctg	gag	atc	aaa	ggc	tcc	acc	336
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Gly	Ser	Thr		
			100					105					110				
agc	ggc	agc	ggt	aag	cca	ggc	tcc	ggc	gaa	ggc	agc	acc	aaa	ggc	gaa	384	
Ser	Gly	Ser	Gly	Lys	Pro	Gly	Ser	Gly	Glu	Gly	Ser	Thr	Lys	Gly	Glu		
			115				120					125					
gtg	aag	ggt	gag	gag	tct	gga	gga	ggc	ttg	gtg	caa	cct	gga	gga	tcc	432	
Val	Lys	Val	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser		
			130				135					140					
atg	aaa	ctc	tcc	tgt	gtt	gtc	tct	gga	ttc	act	ttc	ggt	aat	tac	tgg	480	
Met	Lys	Leu	Ser	Cys	Val	Val	Ser	Gly	Phe	Thr	Phe	Gly	Asn	Tyr	Trp		
					150					155					160		
atg	aac	tgg	gtc	cgc	cag	tct	cca	gag	aag	ggg	ctt	gag	tgg	att	gca	528	
Met	Asn	Trp	Val	Arg	Gln	Ser	Pro	Glu	Lys	Gly	Leu	Glu	Trp	Ile	Ala		
				165					170					175			
gaa	att	aga	ttg	aaa	tcc	aat	aat	ttt	gca	aga	tat	tat	gcg	gag	tct	576	
Glu	Ile	Arg	Leu	Lys	Ser	Asn	Asn	Phe	Ala	Arg	Tyr	Tyr	Ala	Glu	Ser		
			180					185					190				
gtg	aaa	ggg	agg	ttc	acc	atc	tca	aga	gat	gat	tcc	aaa	agt	agt	gtc	624	
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Ser	Val		
			195				200					205					
tac	ctg	caa	atg	atc	aac	cta	aga	gct	gaa	gat	act	ggc	att	tat	tac	672	
Tyr	Leu	Gln	Met	Ile	Asn	Leu	Arg	Ala	Glu	Asp	Thr	Gly	Ile	Tyr	Tyr		
			210				215				220						
tgt	acc	agt	tat	ggt	aac	tac	gtt	ggg	cac	tat	ttt	gac	cac	tgg	ggc	720	
Cys	Thr	Ser	Tyr	Gly	Asn	Tyr	Val	Gly	His	Tyr	Phe	Asp	His	Trp	Gly		
					230					235					240		
caa	ggc	acc	act	ctc	acc	gtc	tcc	tca	gct	agc	ggt	ggc	ggt	ggc	tcc	768	
Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Ser	Gly	Gly	Gly	Gly	Ser		
				245					250					255			
ggt	cta	gac	acc	gtg	agc	ttt	agc	act	aaa	ggt	gcc	act	tat	att	acc	816	
Gly	Leu	Asp	Thr	Val	Ser	Phe	Ser	Thr	Lys	Gly	Ala	Thr	Tyr	Ile	Thr		
			260					265					270				
tac	gtg	aat	ttc	ttg	aat	gag	cta	cga	gtt	aaa	ttg	aaa	ccc	gaa	ggt	864	
Tyr	Val	Asn	Phe	Leu	Asn	Glu	Leu	Arg	Val	Lys	Leu	Lys	Pro	Glu	Gly		
			275				280					285					
aac	agc	cat	gga	atc	cca	ttg	ctg	cgc	aaa	aaa	tgt	gat	gat	cct	gga	912	
Asn	Ser	His	Gly	Ile	Pro	Leu	Leu	Arg	Lys	Lys	Cys	Asp	Asp	Pro	Gly		
			290				295				300						
aag	tgt	ttc	gtt	ttg	gta	gcg	ctt	tca	aat	gac	aat	gga	cag	ttg	gcg	960	
Lys	Cys	Phe	Val	Leu	Val	Ala	Leu	Ser	Asn	Asp	Asn	Gly	Gln	Leu	Ala		
					310					315					320		
gaa	ata	gct	ata	gat	gtt	aca	agt	gtt	tat	gtg	gtg	ggc	tat	caa	gta	1008	
Glu	Ile	Ala	Ile	Asp	Val	Thr	Ser	Val	Tyr	Val	Val	Gly	Tyr	Gln	Val		

325	330	335	
aga aac aga tct tac ttc ttt aaa gat gct cca gat gct gct tac gaa			1056
Arg Asn Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu			
340	345	350	
ggc ctc ttc aaa aac aca att aaa aca aga ctt cat ttt ggc ggc agc			1104
Gly Leu Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser			
355	360	365	
tat ccc tcg ctg gaa ggt gag aag gca tat aga gag aca aca gac ttg			1152
Tyr Pro Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu			
370	375	380	
ggc att gaa cca tta agg att ggc atc aag aaa ctt gat gaa aat gcg			1200
Gly Ile Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala			
385	390	395	400
ata gac aat tat aaa cca acg gag ata gct agt tct cta ttg gtt gtt			1248
Ile Asp Asn Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val			
405	410	415	
att caa atg gtg tct gaa gca gct cga ttc acc ttt att gag aac caa			1296
Ile Gln Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln			
420	425	430	
att aga aat aac ttt caa cag aga att cgc ccg gcg aat aat aca atc			1344
Ile Arg Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile			
435	440	445	
agc ctt gag aat aaa tgg ggt aaa ctc tcg ttc cag atc cgg aca tca			1392
Ser Leu Glu Asn Lys Trp Gly Lys Leu Ser Phe Gln Ile Arg Thr Ser			
450	455	460	
ggt gca aat gga atg ttt tcg gag gca gtt gaa ttg gaa cgt gca aat			1440
Gly Ala Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn			
465	470	475	480
ggc aaa aaa tac tat gtc acc gca gtt gat caa gta aaa ccc aaa ata			1488
Gly Lys Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile			
485	490	495	
gca ctc ttg aag ttc gtc gat aaa gat cct aaa taatga			1527
Ala Leu Leu Lys Phe Val Asp Lys Asp Pro Lys			
500	505		

<210> 11

<211> 507

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic

<400> 11

Met	Thr	Asp	Ile	Val	Met	Thr	Gln	Ser	Gln	Lys	Phe	Met	Ser	Thr	Ser
1				5			10						15		

Glu Ile Ala Ile Asp Val Thr Ser Val Tyr Val Val Gly Tyr Gln Val
 325 330 335
 Arg Asn Arg Ser Tyr Phe Phe Lys Asp Ala Pro Asp Ala Ala Tyr Glu
 340 345 350
 Gly Leu Phe Lys Asn Thr Ile Lys Thr Arg Leu His Phe Gly Gly Ser
 355 360 365
 Tyr Pro Ser Leu Glu Gly Glu Lys Ala Tyr Arg Glu Thr Thr Asp Leu
 370 375 380
 Gly Ile Glu Pro Leu Arg Ile Gly Ile Lys Lys Leu Asp Glu Asn Ala
 385 390 395 400
 Ile Asp Asn Tyr Lys Pro Thr Glu Ile Ala Ser Ser Leu Leu Val Val
 405 410 415
 Ile Gln Met Val Ser Glu Ala Ala Arg Phe Thr Phe Ile Glu Asn Gln
 420 425 430
 Ile Arg Asn Asn Phe Gln Gln Arg Ile Arg Pro Ala Asn Asn Thr Ile
 435 440 445
 Ser Leu Glu Asn Lys Trp Gly Lys Leu Ser Phe Gln Ile Arg Thr Ser
 450 455 460
 Gly Ala Asn Gly Met Phe Ser Glu Ala Val Glu Leu Glu Arg Ala Asn
 465 470 475 480
 Gly Lys Lys Tyr Tyr Val Thr Ala Val Asp Gln Val Lys Pro Lys Ile
 485 490 495
 Ala Leu Leu Lys Phe Val Asp Lys Asp Pro Lys
 500 505